

Genetic Host and Environmental

OXIDOREDUCTASE 1 (NQO1) GENOTYPES AND LUNG-RELATED CANCERS OF THE UPPER AERODIGESTIVE TRACT

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Involved in the metabolism of polycyclic aromatic hydrocarbons in tobacco smoke. Recently, a variant allele of the NQO1 gene has been found to be associated with a complete loss of function of the enzyme. We studied the potential effect of this polymorphism in lung and UAT cancers. One hundred and twenty one patients with cancer of the oral cavity/pharynx, 129 patients with cancer of the larynx, and 129 controls, all Caucasian smokers, were included. Genotyping was performed by a PCR-based method. Cancer risks were estimated by adjusting for sex, age, smoking and alcohol consumption. Heterozygous or homozygous variant genotypes were associated with a higher risk for neither oral/pharynx cancers (OR=2.3, 95%CI=0.6-8.2, respectively) nor larynx cancer (OR=2.1 and OR=1.1, 95%CI=0.2-5.9, respectively) compared to homozygous wild-type genotypes. Moreover, the genotype was not associated with smoking habits. Thus, our study does not support the NQO1 polymorphism in smoking-related UAT

ADENOCARCINOMA: HISTOLOGY, TOBACCO SMOKE EXPOSURE, AND GENETIC HOST FACTORS

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Adenocarcinoma became the most common type of lung cancer in the US, and a similar change has been seen in other countries. In Finland, a 500% increase has occurred in lung cancer and the increase in the incidence of lung adenocarcinoma is higher than among men. We investigated 118 adenocarcinoma cases using p53 mutation as a biomarker. In 29% of the female cases were mutated. When adjusted for exposure, 0% of non-smokers, 48% of ex-smokers,

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Several investigators have analyzed various smoke related aromatic amines and polycyclic aromatic amines and demonstrated an inverse relationship between pH and reactivity or mutagenicity. Using the Ames test, our initial investigation testing the urine of ten smokers and non-smokers exhibited a trend toward a direct relationship. To confirm the significance of these results, we have expanded our study population and hypothesize that changing the pH of smokers urine might impact the mutagenic outcome. Using the Ames test, the mutagenic activity of smokers and non-smokers urine was evaluated utilizing the Salmonella typhimurium YG1024 microsuspenstion assay after each urine sample was titrated to a pH of 5.5, 7.0 and 8.2. The data was then analyzed for standard analysis of variance and post hoc multiple comparisons using Fisher's least significant difference method. The 32 smokers included 13 men and 19 women and the 29 non-smokers included 14 men and 15 women. The mean colony count of the smokers ($x=224$) was significantly higher than the non-smokers ($x=83$), with a $p<0.0001$. The mean colony counts per plate for the smokers at a pH of 5.5, 7.0 and 8.2 were 192 (± 98), 231 (± 134) and 249 (± 164) respectively. There was a statistically significant direct relationship between pH and mutagenicity with the greatest benefit observed between a pH of 5.5 and 7.0 ($p=0.0037$). These results represent the first systematic evaluation of smokers urine demonstrating that urine adjusted to a neutral or basic pH resulted in increased mutagenicity. This relationship may contribute to subsequent risk of bladder cancer in smokers.

#146 BIOLOGICAL MONITORING OF THE TOBACCO SMOKE-RELATED EXPOSURE TO ACROLEIN. Gerhard Scherer, G. Krause, D. Mascher, and E. Schmid, Analytisch-Biologisches Forschungslabor, Munchen, Germany, and Institute of Analytical Chemistry, Univ of Vienna, Vienna, Austria

Acrolein is a suspected human carcinogen. Non-occupational exposure is due to tobacco smoke, automobile exhaust, burning fatty food, cyclophosphamide treatment, and also endogenous formation. 3-Hydroxypropylmercapturic acid (HPMA) is an urinary metabolite of acrolein in animals and men. We determined HPMA by a newly developed method using liquid chromatography with tandem mass spectrometry (LC-MS/MS) in the urine of 41 nonsmokers and 27 smokers. Smokers excreted significantly higher amounts of HPMA than nonsmokers (2.81 vs 0.81 mg/24h). There was a significant correlation between HPMA excretion and daily cigarette consumption ($r = 0.66$) as well as urinary cotinine ($r = 0.60$). Exposure to environmental tobacco smoke (ETS), as determined by questionnaires, nicotine on personal samplers and urinary cotinine, was not found to influence the HPMA excretion. The GST M1 genotype was not related to the HPMA excretion in neither smoker nor nonsmokers, whereas nonsmokers of the GST T1 'Null' genotype tended to show lower excretion rates of HPMA than nonsmokers carrying the gene (0.46 vs 0.88 mg/24h). The difference, however, was not significant.

intensified surveillance, prophylactic surgery. However, the effective identification of familial malignancies remains a challenge. The collection of family history information is generally suggested to be a requirement. To date, few studies have evaluated family history tool in the Identical study was designed to assess the utility of families. Family history data collection of detailed genetic histories have been used to identify cancer seen in the Washington University Cancer Center. The screening family history tool with the detailed genetic histories (records) collected by a genetic counselor of cancer history reporting and recognizing women with increased risk. If effective, this tool could be used for identification of families with hereditary

#149 POLYMORPHISMS IN CYP1A1 AND CYP1B1 AND RISK OF ENDOMETRIAL CANCER. Sara H Olson, Abul K. B. Ambrosone, Fred F. Ambrosone, and Marianne Berwick, Memorial Sloan-Kettering Cancer Center, National Ctr for Toxicological Research

Endometrial cancer is the most common gynecologic cancer to affect women. CYP1A1 and CYP1B1 are potentially important in estrogen metabolism, mostly to the readily methylated estradiol to a long-acting agonist, estrone, which may increase the generation of free radicals. We studied CYP1A1 (ile-val or val-val in exon 3) and CYP1B1 (val-val in codon 432, exon 3) polymorphisms in women with endometrial cancer. We conducted a case-control study of distribution of polymorphisms in women with and without endometrial cancer. Spots from women aged >49 years (controls). Samples were analyzed by PCR amplification and gel electrophoresis were carried out (Cancer Research 1995;55:341). For CYP1A1, 9% of c